```
=> s tuberculosis and
((MTSP1)or(MTSP15)or(MTSP21)or(MTSP23)or(MTSP36)or(MTSP43)or(MTSP47)or(Rv0603)or(Rv1804c)or(Rv12
71c)or(Rv2253)or(Rv0203)or(Rv0617)or(Rv2290))
L1          10 TUBERCULOSIS AND ((MTSP1) OR(MTSP15) OR(MTSP21) OR(MTSP23) OR(MT
               SP36) OR(MTSP43) OR(MTSP47) OR(RV0603) OR(RV1804C) OR(RV1271C)
               OR(RV2253) OR(RV0203) OR(RV0617) OR(RV2290))

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2           6 DUP REM L1 (4 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 6 ANSWERS - CONTINUE? Y/(N):y


L2   ANSWER 1 OF 6  USPATFULL on STN
AN     2005:305853  USPATFULL
TI     High resolution typing system for pathogenic Mycobacterium tuberculosum
IN     Keim, Paul S., Flagtaff, AZ, UNITED STATES
       Spurgiesz, Robert Scott, Flagstaff, AZ, UNITED STATES
       Schupp, James M., Flagstaff, AZ, UNITED STATES
PI     US 2005266492      A1   20051201
AI     US 2005-181587     A1   20050713 (11)
RLI    Division of Ser. No. US 2003-624714, filed on 21 Jul 2003, PENDING
PRAI   US 2002-397224P     20020719 (60)
DT     Utility
FS     APPLICATION
LREP   QUARLES & BRADY LLP, RENAISSANCE ONE, TWO NORTH CENTRAL AVENUE, PHOENIX,
       AZ, 85004-2391, US
CLMN   Number of Claims: 23
ECL    Exemplary Claim: 1
DRWN   3 Drawing Page(s)
LN.CNT 1244
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     MLVA methods for strain discrimination among Mycobacterium tuberculosum
       strains are disclosed. Nine VNTR loci have been identified from genomic
       sequences of Mycobacterium tuberculosum strains and primer pairs
       suitable for amplifying the VNTR by PCR are disclosed. Polymorphisms at
       these loci were used to resolve genotypes into distinct groups. This
       sub-typing scheme is useful for the epidemiological study of
       Mycobacterium tuberculosum and may be applied to the local detection of
       the pathological causative agent of tuberculosum.

L2   ANSWER 2 OF 6  CAPLUS  COPYRIGHT 2005 ACS on STN
AN   2005:11168  CAPLUS
DN   142:234084
TI   Cloning and expression of multiple integral membrane proteins from
     Mycobacterium tuberculosis in Escherichia coli
AU   Korepanova, Alla; Gao, Fei P.; Hua, Yuanzi; Qin, Huajun; Nakamoto, Robert
     K.; Cross, Timothy A.
CS   Department of Chemistry and Biochemistry, Florida State University,
     Tallahassee, FL, 32306, USA
SO   Protein Science (2005), 14(1), 148-158
     CODEN: PRCIEI; ISSN: 0961-8368
PB   Cold Spring Harbor Laboratory Press
DT   Journal
LA   English
AB   Seventy integral membrane proteins from the Mycobacterium
     tuberculosis genome have been cloned and expressed in Escherichia
     coli.  A combination of T7 promoter-based vectors with hexa-His affinity
     tags and BL21 E. coli strains with addnl. tRNA genes to supplement
     sparsely used E. coli codons have been most successful.  The expressed
     proteins have a wide range of mol. wts. and number of transmembrane helixes.
     Expression of these proteins has been observed in the membrane and insol.
     fraction of E. coli cell lysates and, in some cases, in the soluble fraction.
     The highest expression levels in the membrane fraction were restricted to
     a narrow range of mol. wts. and relatively few transmembrane helixes.  In
     contrast, overexpression in insol. aggregates was distributed over a broad
     range of mol. wts. and number of transmembrane helixes.
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RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 6 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 1
AN 2005:167656 BIOSIS
DN PREV200500169558
TI Immunological characterization of novel secreted antigens of Mycobacterium **tuberculosis**.
AU Amor, Y. B.; Shashkina, E.; Johnson, S.; Bifani, P. J.; Kurepina, N.; Kreiswirth, B.; Bhattacharya, S.; Spencer, J.; Rendon, A.; Catanzaro, A.; Gennaro, M. L. [Reprint Author]
CS 225 Warren St, Newark, NJ, 07103, USA
gennaro@phri.org
SO Scandinavian Journal of Immunology, (February 2005) Vol. 61, No. 2, pp. 139-146. print.
ISSN: 0300-9475 (ISSN print).
DT Article
LA English
ED Entered STN: 4 May 2005
Last Updated on STN: 4 May 2005
AB Proteins secreted by Mycobacterium **tuberculosis** are targets of host immune responses and as such are investigated for vaccine and immunodiagnostics development. Computer-driven searches of the M. **tuberculosis** H37Rv genome had previously identified 45 novel secreted proteins. Here, we report the characterization of these antigens in terms of specificity for the M. **tuberculosis** complex and the ability to induce human immune responses. BLAST homology searches and Southern hybridization identified 10 genes that were either specific for the M. **tuberculosis** complex or found in only two nontuberculous mycobacterial species of minor medical significance. Selected recombinant proteins were purified from Escherichia coli cells and tested for the ability to elicit antibody responses in **tuberculosis** patients. Reactivity of the serum panel was '36% with at least one of five novel proteins (**Rv0203**, **Rv0603**, **Rv1271c**, **Rv1804c** and **Rv2253**), 56% with the 38 kDa lipoprotein, a M. **tuberculosis** antigen known to be highly seroreactive, and 68% with a combination of **Rv0203**, **Rv1271c** and the 38 kDa antigen. Thus, at least five novel secreted proteins induce antibody responses during active disease; some of these proteins may increase the sensitivity of serological assays based on the 38 kDa antigen.

L2 ANSWER 4 OF 6 USPATFULL on STN
AN 2004:254370 USPATFULL
TI Comparative mycobacterial geneomics as a tool for identifying targets for the diagnosis, prophylaxis or treatment of mycobacterioses
IN Cole, Stewart, Clamart, FRANCE
PI US 2004197896 A1 20041007
AI US 2004-468356 A1 20040412 (10)
WO 2002-IB1973 20020222
RLI Division of Ser. No. US 2001-270123, filed on 22 Feb 2001, PENDING
DT Utility
FS APPLICATION
LREP FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP, 1300 I STREET, NW, WASHINGTON, DC, 20005
CLMN Number of Claims: 50
ECL Exemplary Claim: 1
DRWN 103 Drawing Page(s)
LN.CNT 2647
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention is directed to a method of selection of purified nucleotidic sequences or polynucleotides encoding proteins or part of proteins carrying at least an essential function for the survival or the virulence of mycobacterium species by a comparative genomic analysis of the sequence of the genome of M. **tuberculosis** aligned on the genome sequence of M. leprae and M. **tuberculosis** and M. leprae marker polypeptides of nucleotides encoding the polypeptides, and methods for using the nucleotides and the encoded polypeptides are disclosed.

L2 ANSWER 5 OF 6 USPATFULL on STN
AN 2004:158567 USPATFULL
TI High resolution typing system for pathogenic Mycobacterium tuberculosum
IN Keim, Paul S., Flagstaff, AZ, UNITED STATES
Spurgiesz, Robert Scott, Flagstaff, AZ, UNITED STATES
Schupp, James M., Flagstaff, AZ, UNITED STATES
PI US 2004121366 A1 20040624
AI US 2003-624714 A1 20030721 (10)
PRAI US 2002-397224P 20020719 (60)
DT Utility
FS APPLICATION
LREP QUARLES & BRADY LLP, RENAISSANCE ONE, TWO NORTH CENTRAL AVENUE, PHOENIX, AZ, 85004-2391
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 1061
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB MLVA methods for strain discrimination among Mycobacterium tuberculosum strains are disclosed. Nine VNTR loci have been identified from genomic sequences of Mycobacterium tuberculosum strains and primer pairs suitable for amplifying the VNTR by PCR are disclosed. Polymorphisms at these loci were used to resolve genotypes into distinct groups. This sub-typing scheme is useful for the epidemiological study of Mycobacterium tuberculosum and may be applied to the local detection of the pathological causative agent of tuberculosum.

L2 ANSWER 6 OF 6 USPATFULL on STN
AN 2003:187811 USPATFULL
TI Comparative mycobacterial genomics as a tool for identifying targets for the diagnosis, prophylaxis or treatment of mycobacterioses
IN Cole, Stewart T., Clamart, FRANCE
PI US 2003129601 A1 20030710
US 2004121322 A9 20040624
AI US 2002-80170 A1 20020222 (10)
PRAI US 2001-270123P 20010222 (60)
DT Utility
FS APPLICATION
LREP FINNEGAN, HENDERSON, FARABOW, GARRETT &, DUNNER LLP, 1300 I STREET, NW, WASHINGTON, DC, 20006
CLMN Number of Claims: 74
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 6691
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention is directed to a method of selection of purified nucleotidic sequences or polynucleotides encoding proteins or part of proteins carrying at least an essential function for the survival or the virulence of mycobacterium species by a comparative genomic analysis of the sequence of the genome of M. **tuberculosis** aligned on the genome sequence of M. leprae and M. **tuberculosis** and M. leprae marker polypeptides of nucleotides encoding the polypeptides, and methods for using the nucleotides and the encoded polypeptides are disclosed.